



## SEQUENCE LISTING

<110> Dunn-Coleman, Nigel  
Langdon, Timothy  
Morse, Phillip

<120> Manipulation of the Phenolic Acid  
Content and Digestibility of Plant Cell Walls by Targeted  
Expression of Genes Encoding Cell Wall Degrading Enzymes

<130> GC648-2

<140> US 09/991,209

<141> 2001-11-16

<150> US 60/249,608

<151> 2000-11-17

<160> 97

<170> FastSEQ for Windows Version 4.0

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<212> DNA

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35     40     45
Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn
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65     70     75     80
Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln
85     90     95
Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys
100    105    110
Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly Trp Val Ser Val
115    120    125
Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val Ser Gln Tyr Pro
130    135    140
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Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp Asn Ile Arg Leu
165    170    175
Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr
180    185    190
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210    215    220
Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr
225    230    235    240
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 <213> Artificial Sequence

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&lt;223&gt; functional PCR product reading frame

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&lt;210&gt; 4

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; inactivated PCR product reading frame

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35

&lt;210&gt; 5

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; retention sequence

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; retention sequence encoding sequence

&lt;400&gt; 6

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33

&lt;210&gt; 7

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; FAE-linker-frameshift sequence

&lt;400&gt; 7

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&lt;210&gt; 8

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; FAE-linker-frameshift sequence

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20 25 30  
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35 40

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<211> 134  
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<213> Hordeum sp.

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35 40 45

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<212> DNA  
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<212> PRT  
<213> Solanum sp.

<220>  
<221> VARIANT  
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<223> Xaa = Any Amino Acid

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 <213> Solanum sp.

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Gly Glu Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu
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<213> Artificial Sequence

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 50             55             60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
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&lt;211&gt; 5337

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; pTP8-5 vector

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<211> 306
<212> PRT
<213> Artificial Sequence

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<220>
<223> pTP8-5 vector

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<221> VARIANT
<222> (1)...(306)
<223> Xaa = Any Amino Acid

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<400> 24

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Ile Arg Pro Val Thr Asp Arg Ala Ala Ala Ser Thr Gln Gly Ile Ser
35          40          45
Glu Asp Leu Tyr Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
50          55          60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
65          70          75          80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
85          90          95
Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
100         105         110
Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
115         120         125
Leu Pro Gln Cys Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
130         135         140
Trp Val Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val
145         150         155         160
Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly
165         170         175
Ala Ser Leu Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
180         185         190
Asn Ile Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
195         200         205
Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr
210         215         220
Thr Gln Tyr Phe Arg Val Thr His Ala Asn Asp Gly Ile Pro Asn Leu
225         230         235         240
Pro Pro Val Glu Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
245         250         255
Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
260         265         270
Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asn Ala His
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Ala Ala
305

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 <211> 5277  
 <212> DNA  
 <213> Artificial Sequence

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 <223> pTP5-1 vector

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<213> Artificial Sequence

<220>

<223> pTP5-1 vector

<221> VARIANT

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<223> Xaa = Any Amino Acid

<400> 26

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      20             25             30
Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp
      35             40             45
Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn
      50             55             60
Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp Asp Ser Ser Lys

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Gln	Asp	Gln	Val	Glu	Ser	Leu	Val	Lys	Gln	Gln	Val	Ser	Gln	Tyr
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Asp	Tyr	Ala	Leu	Thr	Val	Thr	Gly	His	Xaa	Leu	Gly	Ala	Ser	Leu
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Ala	Leu	Thr	Ala	Ala	Gln	Leu	Ser	Ala	Thr	Tyr	Asp	Asn	Ile	Arg
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Tyr	Thr	Phe	Gly	Glu	Pro	Arg	Ser	Gly	Asn	Gln	Ala	Phe	Ala	Ser
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Arg	Val	Thr	His	Ala	Asn	Asp	Gly	Ile	Pro	Asn	Leu	Pro	Pro	Val
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	290													

&lt;210&gt; 27

&lt;211&gt; 5327

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pTP4a2 vector

&lt;400&gt; 27

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 65           70           75           80
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&lt;223&gt; pGT6 vector

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&lt;223&gt; pJQ4 vector

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&lt;223&gt; pPQ10.1 vector

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&lt;210&gt; 37

&lt;211&gt; 4965

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pJQ3 vector

&lt;400&gt; 37

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&lt;210&gt; 38

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&lt;220&gt;

&lt;223&gt; pUG4 vector

&lt;400&gt; 38

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5295

&lt;210&gt; 39

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pUG4 vector

&lt;221&gt; VARIANT

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&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 39

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Gly Glu Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu
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Asp Glu Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asn
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&lt;211&gt; 5001

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;213&gt; Artificial Sequence

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&lt;223&gt; pTP11-1 vector

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acttagactc	aaaacattta	caaaaacaac	ccctaaagtc	ctaaagccca	aagtgtctatg	4680
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<210> 42

<211> 301

<212> PRT

<213> Artificial Sequence

<220>

<223> pTP11-1 vector

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<222> (1)...(301)

<223> Xaa = Any Amino Acid

<400> 42

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Ile Arg Pro Val Thr Asp Arg Ala Ala Ala Ser Thr Gln Gly Ile Ser
35          40          45
Glu Asp Leu Tyr Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
50          55          60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
65          70          75          80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
85          90          95
Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
100         105         110
Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
115         120         125
Leu Pro Gln Cys Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
130         135         140
Trp Val Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val
145         150         155         160
Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly
165         170         175
Ala Ser Leu Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
180         185         190
Asn Ile Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
195         200         205
Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr
210         215         220
Thr Gln Tyr Phe Arg Val Thr His Ala Asn Asp Gly Ile Pro Asn Leu
225         230         235         240
Pro Pro Val Glu Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
245         250         255
Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
260         265         270
Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asn Ala His

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275                      280                      285  
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 290                      295                      300

<210> 43  
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 <213> Artificial Sequence

<220>  
 <223> actin promoter

<400> 43  
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 agtaaaatat cggtaataaa aggtggccca aagtgaattt tactcttttc tactattata 180  
 aaaattgagg atgttttggt ggtactttga tacgtcattt ttgtatgaat tggtttttaa 240  
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 ttgtaaatac agagggattt gtataagaaa tatcttttaa aaaccatata gctaatttga 360  
 cataattttt gagaaaaata tatattcagg cgaattccac aatgaacaat aataagatta 420  
 aaatagcttg cccccgttg agcgatgggt attttttcta gtaaaataaa agataaactt 480  
 agactcaaaa catttacaaa aacaacccct aaagtcctaa agcccaaagt gctatgcacg 540  
 atccatagca agcccagccc aacccaaccc aacccaaccc accccagtgc agccaactgg 600  
 caaatagtct ccacccccgg cactatcacc gtgagttgtc cgcaccaccg cacgtctcgc 660  
 agccaaaaaa aaaaaaagaa agaaaaaaa gaaaaagaaa aacagcaggt ggggtccgggt 720  
 cgtggggggc ggaaaagcga ggaggtatcgc gagcagcgac gagggccggc cctccctccg 780  
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 cccaacccta ccaccaccac caccaccacc tcctcccccc tcgctgcccg acgacgagct 900  
 cctccccctt cccccctcgc cgccgcccgt aaccaccccg cccctctcct ctttctttct 960  
 ccgttttttt tttcgtctcg gtctcgatct ttggccttgg tagtttggtt gggcgagagc 1020  
 ggcttcgtcg ccagatcgg tgcgcgggag gggcgggatc tcgcggtctg cgtctccggg 1080  
 cgtgagtcgg ccggtatcct cgcggggaat ggggctctcg gatgtagatc ttctttcttt 1140  
 cttctttttg tggtagaatt tgaatccctc agcattgttc atcggtagtt tttcttttca 1200  
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<210> 44  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> aleurain-NPIR delete structure

<400> 44  
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 Ala Ala Val Ala Val Ala Ser Ser Arg Ala Ala  
 20                      25

<210> 45  
 <211> 93  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> aleurain-NPIR delete structure encoding sequence

<400> 45  
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 gccgtcgccg tcgcctcctc ccgcgcggcc gcc 93

<210> 46  
 <211> 873  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> SEE1 (senescence enhanced) promoter

<400> 46  
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 ctagatagca cagccacagc acctacagga gtgcgacact tgtggactgt agtagtggtg 180  
 gagacggagc tctttcctac ctccctgacgt tgccgccgtt gtccattcca acggcatcac 240  
 tctcaaccaa tcacgcgctc ccaacaaaat atcgtccccc atgtcttggc ggagagagag 300  
 tacatacatg ctgtcgcgcc gtttttgtct gaatctcgtc tccactggcc aatcagctca 360  
 gctcccggga gctcactcat tcaagatccc atcgtcgtcg tcacccctgg cgtcatggga 420  
 tggaaaagaa cctccgttgc tcggatgagt cagccatata cccgaacaga gtactgcaag 480  
 ataaccat tccagattccc ccaatagaga aagtatagca tgctttcggg ttttgtttg 540  
 cttaattgac tttatTTTTTg ttggagttga atgctgattt gttgtgtaaa atgcccaacc 600  
 atctgaatat cgagacggat aataggctgg ctaattaatt tatagcaaga ttctgtagt 660  
 cacatcgcaa atatctttct gggcattaca gctggaggct tcatcagcct gaaacactct 720  
 gcagagcctg aagcaagtgg tgaagcgtgg cgatgagatg ggtataaaac ccccggcacc 780  
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<210> 47  
 <211> 39  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> SEE1 promoter plus vacuolar aleurain signal/NPIR  
 sequence

<400> 47  
 Met Ala His Gly Arg Ile Leu Phe Leu Ala Leu Ala Val Leu Ala Thr  
 1 5 10 15  
 Ala Ala Val Ala Ala Ala Ser Leu Ala Asp Ser Asn Pro Ile Arg Pro  
 20 25 30  
 Val Thr Glu Arg Ala Ala Ala  
 35

<210> 48  
 <211> 987  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> SEE1 promoter plus vacuolar aleurain signal/NPIR  
 encoding sequence

<221> misc\_feature  
 <222> (1)...(987)  
 <223> n = A,T,C or G

<400> 48  
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 ctagatagca cagccacagc acctacagga gtgcgacact tgtggactgt agtagtggtg 180

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tctcaaccaa	tcacgcgctc	ccaacaaaat	atcgcccccc	atgtcttggc	ggagagagag	300
tacatacatg	ctgtcgcgcc	gtttttgtct	gaatctcgtc	tccactggcc	aatcagctca	360
gctcccggga	gctcactcat	tcaagatccc	atcgctcgtc	tcacccctgg	cgatcatggg	420
tggaagagaa	cctccgttgc	tcggatgagt	cagccatata	cccgaacaga	gtactgcaag	480
ataacccaat	tcagattccc	ccaatagaga	aagtatagca	tgctttcggg	ttttgtttgg	540
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atctgaatat	cgagacggat	aataggctgg	ctaattaatt	tatagcaaga	ttctgtagtg	660
cacatcgcaa	atatctttct	gggcattaca	gctggaggct	tcatacagct	gaaacactct	720
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gtaaaatact	gttgcccaact	cgccggcgag	atggcccacg	gccgcatact	cttcttggcg	900
ctcgccgtct	tggccaccgc	cgcggtggcc	gccgcatact	tggcgggactc	caacccgatc	960
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<210> 49

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 49

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<210> 50

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 50

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<210> 51

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 51

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<210> 52

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 52

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<210> 53

<211> 325  
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<220>  
 <223> amplified nos terminator sequence from pMA406  
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 tatcatataa tttctgttga attacgttaa gcatgtaata attaacatgt aatgcatgac 180  
 gttattttatg agatggggtt ttatgattag agtcccgcga ttatacattt aatacgcgat 240  
 agaaaacaaa atatagcgcg caaactagga taaattatcg cgcgcggtgt catctatgtt 300  
 actagatcga taagcttcta gatct 325

<210> 54  
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 <212> DNA  
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<220>  
 <223> primer

<400> 54  
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 ttcaaacatt tg 72

<210> 55  
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 <212> DNA  
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<220>  
 <223> primer

<400> 55  
 aagactgcag accatggcgg 20

<210> 56  
 <211> 40  
 <212> DNA  
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<220>  
 <223> primer

<400> 56  
 agatctagaa gcttatcgat ctagtaacat agatgacacc 40

<210> 57  
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<220>  
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<400> 57  
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<210> 58  
 <211> 36  
 <212> DNA  
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<400> 58  
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<210> 59  
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<210> 60  
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 <223> Accl site

<400> 60  
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<210> 61  
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<210> 62  
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<220>  
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<400> 62  
 aaccatggcg gccgcgcgct cggtagcggg ccggat 36

<210> 63  
 <211> 29  
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 <400> 63  
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 <210> 64  
 <211> 31  
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 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
 <400> 65  
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 <210> 66  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer  
  
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 <210> 67  
 <211> 33  
 <212> DNA  
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 <210> 68  
 <211> 54  
 <212> DNA  
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 <220>  
 <223> primer  
  
 <400> 68



gcgacggcga cggcggccgt ggccagcacg gcgagcgcca ggaggaggac gcgg 54

<210> 69  
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<400> 69  
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<210> 70  
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<220>  
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<400> 70  
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<210> 71  
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<220>  
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<400> 71  
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<210> 72  
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<210> 73  
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<220>  
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<212> DNA  
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<220>  
 <223> primer

<400> 74  
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<210> 75  
 <211> 34  
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<400> 75  
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<210> 76  
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 <212> DNA  
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<400> 76  
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 a 61

<210> 77  
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<220>  
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<400> 77  
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<210> 78  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 78  
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<210> 79  
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<220>

<223> primer

<400> 79

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37

<210> 80

<211> 43

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<210> 81

<211> 39

<212> DNA

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<220>

<223> primer

<400> 81

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<210> 82

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 82

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47

<210> 83

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 83

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32

<210> 84

<211> 8

<212> DNA

<213> Oryza sp.

<400> 84

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8

<210> 85

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> KDEL fusion peptide

<400> 85

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1 5

<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> designated KDEL fusion peptide

<400> 86

Glu Pro Leu Lys Asp Glu Leu  
1 5

<210> 87

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> frameshifted terminal peptide

<400> 87

Glu Thr Thr Glu Gly  
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<210> 88

<211> 27

<212> PRT

<213> Aspergillus niger

<400> 88

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Gly His Ala Leu Ala Ala Ser Thr Gln Gly Ile  
20 25

<210> 89

<211> 9

<212> PRT

<213> Aspergillus niger

<400> 89

Met Ala Ala Ala Ser Thr Gln Gly Ile  
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<210> 90

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> ER retention vector

<400> 90

Lys Pro Leu Lys Asp Glu Leu  
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<210> 91

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> c-terminal targeting sequence

<400> 91

Pro Val Ala Ala Ala  
1 5

<210> 92

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 92

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55

<210> 93

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> ferulic esterase end

<400> 93

Cys Thr Trp Pro Val Ala Ala Ala  
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<210> 94

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> pTP4a2 vector

<400> 94

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		20						25				30			
Ser	Arg	Leu	Val	Glu	Met	Ala	Thr	Ile	Ser	Gln	Ala	Ala	Tyr	Ala	Asp
		35				40					45				
Leu	Cys	Asn	Ile	Pro	Ser	Thr	Ile	Ile	Lys	Gly	Glu	Lys	Ile	Tyr	Asn
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Ser	Gln	Thr	Asp	Ile	Asn	Gly	Trp								
65						70									

<210> 95  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> protein encoded by functional reading frame

<400> 95  
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 Leu

<210> 96  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> protein encoded by inactivated reading frame

<400> 96  
 Tyr Ala Leu Thr Val Thr Gly His Ala Leu Gly Ala Ser Leu Ala Ala  
 1 5 10 15  
 Leu

<210> 97  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> retention sequence

<400> 97  
 Lys Asp Glu Leu  
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